



## Perspective

Different strategies for producing naturally soluble form of common cytokine receptor  $\gamma$  chain

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## ABSTRACT

The common cytokine receptor  $\gamma$  chain ( $\gamma_c$ ) plays an essential role in regulating lymphoid homeostasis. In fact, alteration of this gene causes severe immunodeficiency in humans and animals. Although soluble  $\gamma_c$  ( $s\gamma_c$ ) was identified in the late 1990s, much remains unknown about its production. This study describes various mechanisms underlying the generation of  $s\gamma_c$  isoforms in different species. Our data demonstrate that mouse  $\gamma_c$  and the avian ortholog  $\gamma_c$ -a did not generate  $s\gamma_c$ . Moreover, two mouse isoforms, CRA-a and m $\gamma_c$ -b, encoded by transcripts lacking a transmembrane region by alternative splicing, did not yield  $s\gamma_c$ . However, in ducks,  $s\gamma_c$  was produced from a  $\gamma_c$ -b transcript lacking a transmembrane region by alternative splicing. In chickens,  $s\gamma_c$  was produced in normal cells and cell lines by proteolytic shedding of the  $\gamma_c$ -b isoform containing intron 5, which displayed a relatively high probability of proteolytic cleavage of the ectodomain. This shedding was suppressed by leupeptin, serine and cysteine protease inhibitor. Compared to the chicken ortholog  $\gamma_c$ -a, expression of  $\gamma_c$ -b mRNA was differentially regulated according to tissue type, developmental stage, and antigen stimulation. These data demonstrate several mechanisms for producing  $s\gamma_c$  and suggest a potential role for  $s\gamma_c$  in avian lymphoid homeostatic responses to environmental antigens.

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## 1. Introduction

The common cytokine receptor  $\gamma$  chain ( $\gamma_c$ ), which is also known as interleukin-2 receptor (IL-2R $\gamma$ ) or CD132, is a subunit shared by receptors for IL-2, IL-4, IL-7, IL-9, IL-15, and IL-21. A member of the type 1 cytokine receptor superfamily,  $\gamma_c$  is composed of four  $\alpha$ -helical bundles, characteristic spacing of four conserved cysteine residues, and a WSXWS motif (Alves et al., 2007; Malek and Castro, 2010; Rochman et al., 2009).  $\gamma_c$  expression is observed on B cells, T cells, natural killer (NK) cells, monocytes/macrophages, granulocytes, and dendritic cells.  $\gamma_c$  forms heterodimeric or heterotrimeric complexes with specific receptor subunits, resulting in increased ligand affinity, receptor internalization, and signal transduction (Rochman et al., 2009; Sugamura et al., 1995; Walsh, 2012). The cytoplasmic

domain of  $\gamma_c$  contributes to intracellular signaling by interacting with Janus kinase (JAK) and signal transducer and activator of transcription (STAT) proteins, which ultimately regulate lymphocyte development, proliferation, and homeostasis in innate and adaptive immunity (Overwijk and Schluns, 2009; Vigliano et al., 2012; Walsh, 2012). Not surprisingly, alteration of the gene encoding  $\gamma_c$  causes X-linked severe combined immunodeficiency in humans and animals (Henthorn et al., 1994; Kovanen and Leonard, 2004; Noguchi et al., 1993).

The soluble forms of several cytokine and growth factor receptors play key roles in regulating cytokine-dependent biological activities by binding target ligands present in the bodily fluids of humans and animals (Fernandez-Botran et al., 1996; Levine, 2008; Rose-John and Heinrich, 1994). Two major mechanisms have been described for producing these soluble cytokine receptors, namely sheddase-mediated proteolytic cleavage of membrane-associated receptors and synthesis by alternative splicing of mRNA transcripts lacking a transmembrane region (Fernandez-Botran et al., 1996; Levine, 2008). While the soluble IL-6 receptor (sIL-6R) can be produced via both these mechanisms in humans, sIL-6R can only

Abbreviations:  $\gamma_c$ , common cytokine receptor  $\gamma$  chain;  $s\gamma_c$ , soluble  $\gamma_c$ ; ch $\gamma_c$ -a, chicken  $\gamma_c$ -a; ch $\gamma_c$ -b, chicken  $\gamma_c$ -b; du $\gamma_c$ -a, duck  $\gamma_c$ -a; du $\gamma_c$ -b, duck  $\gamma_c$ -b; m $\gamma_c$ , mouse  $\gamma_c$ .

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be generated by proteolytic cleavage in mice (Rose-John, 2012). In addition, alternative splicing alone has been shown to generate several soluble CD40 receptors (Eshel et al., 2008).

The gene encoding  $\gamma_c$  is composed of eight exons and seven introns, resulting in a 64-kDa transmembrane glycoprotein (Min et al., 2002; Sugamura et al., 1995). Soluble  $\gamma_c$  ( $s\gamma_c$ ), in a limited number of cases, has been detected in sera from patients with inflammatory bowel disease (Nielsen et al., 1998), in synovial fluid from rheumatoid joints (Nishio et al., 2001), in sera from certain inbred mice, and stimulated immune cells (Meissner et al., 2001). However,  $s\gamma_c$  forms were not detected in supernatants from normal and activated lymphocyte cultures or in sera from healthy individuals and patients with various disorders (Lundin et al., 2002). Despite extensive knowledge about the function of  $\gamma_c$  at the molecular level, the mechanisms leading to the natural production of  $s\gamma_c$  remain to be elucidated. Our previous studies revealed that avians express two different  $\gamma_c$  transcripts on normal cells due to alternative splicing, resulting in  $ch\gamma_c$ -b containing an in-frame 78 bp insertion between Gly-222 and Val-223 of the  $ch\gamma_c$ -a sequence and in  $du\gamma_c$ -b containing a frame-switching 88-bp insertion which produced a receptor molecule lacking a transmembrane region (Jeong et al., 2011; Min et al., 2002). These findings suggest that different species produce  $s\gamma_c$  isoforms via different mechanisms. Here, we demonstrate proteolytic shedding and alternative splicing as mechanisms for the generation of naturally occurring  $s\gamma_c$  in normal conditions.

## 2. Materials and methods

### 2.1. Animals, treatments, and infection

Eggs from ROSS chickens were obtained from Samhwa (Chungnam, Korea) and hatched at the Gyeongsang National University. Chickens were given unlimited access to feed and water. Constant light was provided for the duration of the experiments. Ten-day-old chickens were orally infected with  $1 \times 10^4$  sporulated *E. tenella* oocysts (Korean isolate 291-7) (Jeong et al., 2012) and transferred to disposable cages (Yoo et al., 2011). *E. tenella* oocysts were cleaned by flotation on 5.25% sodium hypochlorite and washed three times with phosphate-buffered saline (PBS). Spleen and cecal tonsil were collected on days 0, 1, 4, 7, and 10 post-infection. For antigen inoculation, 3-week old chickens were injected with LPS (500  $\mu$ g/kg) or ConA (500  $\mu$ g/kg) via wing vein and spleen tissues collected 4 h later. Control chickens were inoculated with the same volume of PBS. Dexamethasone inoculation was performed as previously described (Kong et al., 2002). Briefly, 4-week-old chickens were administered dexamethasone (5 mg/kg) daily via intramuscular injection into the thigh for 1 week. Thereafter, spleen and thymus were collected. All animal protocols were approved by the Institutional Animal Care and Use Committee (IACUC) at Gyeongsang National University, Jinju, Republic of Korea (Approval Number: GNU-120615-C0022).

### 2.2. Cell culture

The chicken lymphoblast cell lines CU91 and CU205 (Schat et al., 1992), chicken B cell line DT40 (Baba et al., 1985), macrophage cell line HD11 (Beug et al., 1979), COS-7 cells, splenic lymphocytes, and peripheral blood mononuclear cells (PBMC) were cultured in Dulbecco's modified Eagle's medium (DMEM) (Hyclone, USA) supplemented with 10% fetal bovine serum (FBS) and penicillin/streptomycin (10,000 unit/ml) (Hyclone) at 37 °C or 41 °C in 5% CO<sub>2</sub>. Splenic lymphocytes were resuspended to  $4 \times 10^6$  cells/ml and stimulated with 25  $\mu$ g/ml poly I:C, 10  $\mu$ g/ml lipopolysaccharide (LPS from *E. coli*, 0111:B4), 10  $\mu$ g/ml lipoteichoic acid (LTA) (all purchased from Sigma-Aldrich, Germany), or 10  $\mu$ g/ml concanavalin (ConA) (Amersham Bioscience, Sweden) for 0, 4, 8 and 24 h.

### 2.3. Plasmid construction and cell transfection

Chicken and duck  $\gamma_c$ -a and  $\gamma_c$ -b (Jeong et al., 2011; Min et al., 2002) DNA, as well as mouse  $\gamma_c$  DNA (Kumaki et al., 1993) were isolated by PCR from single-stranded cDNA synthesized from splenic lymphocyte mRNA using gene-specific primers with FLAG- or Myc-tagging sequence (Supplementary Table S1). Due to no available antibody against interesting proteins, adding the FLAG- or Myc-tag allows detection of the proteins by Western blotting. PCR products were digested with *Hind*III and *Eco*RI, cloned into the corresponding restriction sites of pcDNA 3.1 (Invitrogen, USA), and verified by DNA sequencing. COS-7 cells were transiently transfected with 10  $\mu$ g of  $\gamma_c$ -expressing construct or empty vector (negative control) using Lipofectamine 2000 Reagent (Invitrogen) according to the manufacturer's protocol. Transfected cells were cultured for 24 to 48 h in serum-free DMEM at 37 °C in 5% CO<sub>2</sub>, and when necessary, treated with PNGase-F (NEB, USA), chloroquine, Brefeldin A (an inhibitor of protein transport from the endoplasmic reticulum to Golgi), and protease inhibitors (Sigma Aldrich, USA) as described.

### 2.4. Western blotting

Cells were lysed with ice-cold buffer (50 mM Tris-HCl (pH 7.5), 150 mM NaCl, 1% sodium deoxycholate, 2 mM EDTA, 0.1 SDS, and 1% Triton X-100) containing 1% Halt protease inhibitor cocktail (Thermo Fisher Scientific, USA) and centrifuged at 12,000 rpm for 30 min at 4 °C to remove debris. Culture supernatants were centrifuged to remove cell debris and concentrated up to 10-fold using centrifugal filters (Merck Millipore LTD, Germany). Cell lysates and supernatants were mixed with an equal volume of reducing sample buffer (0.125 M Tris-HCl (pH 6.8), 4% SDS, 20% glycerol, 10% 2-mercaptoethanol, and 0.004% bromophenol blue), boiled for 5 min, resolved on 10% SDS-polyacrylamide gels, and then transferred to polyvinylidene difluoride (PVDF) membranes (Biorad, USA). Membranes were blocked with PBS containing 5% nonfat dry milk for 2 h at room temperature and incubated with the appropriate primary antibody at 4 °C overnight.  $\gamma$ M1–11 monoclonal antibody against the extracellular domain of  $ch\gamma_c$  (Min et al., 2002), glyceraldehyde 3-phosphate dehydrogenase (GAPDH) antibody (Bioworld, USA), as well as FLAG and Myc antibodies (Cell Signaling Technology, USA) were used. After washing three times with PBS containing 0.1% Tween 20 (PBS-T), membranes were incubated with horseradish peroxidase-conjugated goat anti-mouse IgG antibody (Promega, USA) in PBS containing 1% nonfat dry milk for 40 min at room temperature. Membranes were washed five times with PBS-T and then five times with distilled water, visualized using an Enhanced Chemiluminescence Kit and Western Blotting Detection Reagent (GE Healthcare Life Sciences, USA), and exposed to X-ray film (AGFA, Belgium) as described previously (Jeong et al., 2012).

### 2.5. Quantitative real-time PCR (qRT-PCR)

Tissues and cells were homogenized in RiboEx reagent (GeneAll, Korea) and total RNA was isolated using RNeasy spin columns followed by DNase treatment (Qiagen, Germany). Total RNA was measured using a nano spectrophotometer (Optizen, Korea) and cDNA synthesis was performed using the Quantitect Reverse Transcription kit (Qiagen). Real-time PCR was performed on a CFX96 real-time PCR system (Bio-Rad) with SYBR Green (Bioneer, Korea) using the primers listed in Supplementary Table S1. A melting curve was obtained at the end of each run to verify the presence of a single amplification product and no primer dimers. The relative expression levels of individual transcripts were normalized to that of  $\beta$ -actin with Bio-Rad CFX software. The gene expression levels were quantified using the comparative  $\Delta$ Ct method with  $\beta$ -actin as a reference

for normalization. The fold change in expression of each gene examined from *E. tenella*-infected chickens was calculated relative to their expression levels in the same tissues of uninfected chickens as described previously (Jeong et al., 2012).

## 2.6. Statistical analysis

Statistical significance was calculated using the Student's t-test or one-way ANOVA followed by the Dunnett multiple comparison test using InStat® software (GraphPad, USA). Data were considered statistically significant if  $P < 0.05$ , and are expressed as the mean  $\pm$  standard error.

## 3. Results

### 3.1. Natural production of $s\gamma_c$ forms by proteolysis in chickens

To address the possibility of a cleavage mechanism, 22-mer peptides generated from mammalian  $\gamma_c$  and avian  $\gamma_c$ -a, along with 36-mer peptides from avian  $\gamma_c$ -b, were analyzed using a predictive program (NetChop 3.0) for proteasomal cleavage sites (Nielsen et al., 2005). The highest ranked potential cleavage sites (threshold set at 0.5) were observed at the  $\gamma_c$  C-terminus of 22-mer peptides in human, mouse, and cow (Fig. 1A). However, different patterns of peptide cleavage were observed when the algorithm was applied to 22-mer peptides from the chicken ortholog  $\gamma_c$ -a (Fig. 1B) and quail ortholog  $\gamma_c$ -a (data not shown) (Jeong et al., 2011). Compared to mammalian  $\gamma_c$  and avian  $\gamma_c$ -a, a greater probability of cleavage was observed in the chicken isoform  $\gamma_c$ -b (Fig. 1B) and quail isoform  $\gamma_c$ -b (data not shown), both of which possess an additional eight cleavage site due to the presence of intron 5 by alternative splicing (Fig. 1A and 1B). Moreover, intron 5 in  $\gamma_c$ -b changed the predicted probability of cleavage at certain sites. More specifically, the probability of cleavage at positions G222, V223, and A224 were 0.03, 0.40, and 0.07 in  $\gamma_c$ -a but were 0.53, 0.87, and 0.92 in  $\gamma_c$ -b, respectively (Fig. 1B). A similar effect was observed in quail  $\gamma_c$ -b (data not shown). These data suggest that alternatively spliced isoforms ( $\gamma_c$ -b) with 26 amino acids inserted into the juxtamembrane region augment the probability of proteolytic cleavage.

To test this hypothesis, constructs expressing C-terminal FLAG-tagged murine  $\gamma_c$  ( $m\gamma_c$ ) and  $\gamma_c$ -a, and Myc-tagged  $\gamma_c$ -b were transiently transfected into COS-7 cells and their expression was assessed by Western blot analysis (Fig. 1C). Cell lysates transfected with  $m\gamma_c$  and  $\gamma_c$ -a constructs produced bands at 64 and 52 kDa, respectively, whereas  $\gamma_c$ -b displayed two major bands corresponding to 19 and 55 kDa. Densitometric analysis of the two  $\gamma_c$ -b bands revealed that the intensity of the lower band was 1.5- to 2.5-fold greater than the upper band although some variability was observed. Collectively, these data indicate that  $\gamma_c$ -b, due to insertion of 26 amino acids with a molecular weight 2.8 kDa, is readily cleaved in unstimulated COS-7 cells. This result, unlike  $m\gamma_c$  and  $\gamma_c$ -a, which show little basal shedding, suggests that, if these results could be extrapolated to the natural situation, chickens could generate naturally occurring  $s\gamma_c$  in the form of  $\gamma_c$ -b.

We next investigated whether the naturally occurring  $s\gamma_c$  originated from  $\gamma_c$ -b. Supernatant from COS-7 cells transfected with  $\gamma_c$ -a and  $\gamma_c$ -b was analyzed by Western blot using a monoclonal antibody ( $\gamma M1-11$ ) directed against the extracellular domain of  $\gamma_c$  (Min et al., 2002). An approximately 40 kDa protein was detected in the supernatant of COS-7 cells transfected with  $\gamma_c$ -b, but not  $\gamma_c$ -a or empty vector alone (Fig. 1D). This molecular weight protein showed a similar size of full-length  $\gamma_c$ -b, which has 42.5 kDa as predicted molecular weight (Min et al., 2002). When the supernatant of COS-7 cells transfected with  $\gamma_c$ -b was treated with peptide-N-glycosidase F (PNGase-F), approximately 26 kDa proteins were observed, showing a much smaller size protein than that

of full-length  $\gamma_c$ -b. These results indicate that the observed secreted  $\gamma_c$ -b represents 26 kDa of  $\gamma_c$ -b with 14 kDa N-linked glycosylation (Fig. 1E). In addition, cell lysates and culture supernatants of COS-7 cells transfected with  $\gamma_c$ -b resulted in minor bands at 22 (Fig. 1C) and 29 kDa (Fig. 1E). These experiments indicate that the naturally occurring  $s\gamma_c$  form is mainly generated from isoform  $\gamma_c$ -b under normal conditions via cleavage at a minimum of two sites within its juxtamembrane region.

Generally, ectodomain shedding of transmembrane receptors at the cell surface occurs by proteolysis. However, studies have also demonstrated intracellular proteolytic cleavage (Keller et al., 2006; Levine, 2008). Previous reports have shown that protease and kinase inhibitors do not suppress ectodomain shedding of  $m\gamma_c$  (Meissner et al., 2001). Following endocytosis, most  $\gamma_c$  is sorted to lysosomes where it is degraded (Hémar et al., 1995). Therefore, we investigated whether the intracellular fragment corresponding to 19 kDa (Fig. 1C) is generated by spontaneous lysis within the lysosomal compartment. COS-7 cells transiently transfected with  $\gamma_c$ -b-expressing constructs were cultured for 24 h and then treated with 200  $\mu$ M chloroquine, an inhibitor of lysosomal activity. As shown in Fig. 2A, chloroquine treatment did not prevent the generation of intracellular  $\gamma_c$ -b fragments. Treatment with brefeldin A also had no effect. These results suggest that  $s\gamma_c$  shedding from  $\gamma_c$ -b is not linked to lysosomal proteolysis or the secretory pathway from the Golgi complex to the cell membrane. Therefore, ectodomain shedding of  $\gamma_c$ -b most likely occurs at the cell surface.

To confirm this, COS-7 cells were transfected with a construct expressing Myc-tagged  $\gamma_c$ -b and then treated with a cocktail of protease inhibitors, including aprotinin, bestatin, E-64, leupeptin, and pepstatin A (Fig. 2B). Of these protease inhibitors, leupeptin specifically inhibited the  $\gamma_c$ -b cleavage in dose-dependent manners (Fig. 2C and 2D). These observations indicate that  $s\gamma_c$  generated from  $\gamma_c$ -b is released via proteolytic cleavage at the cell surface.

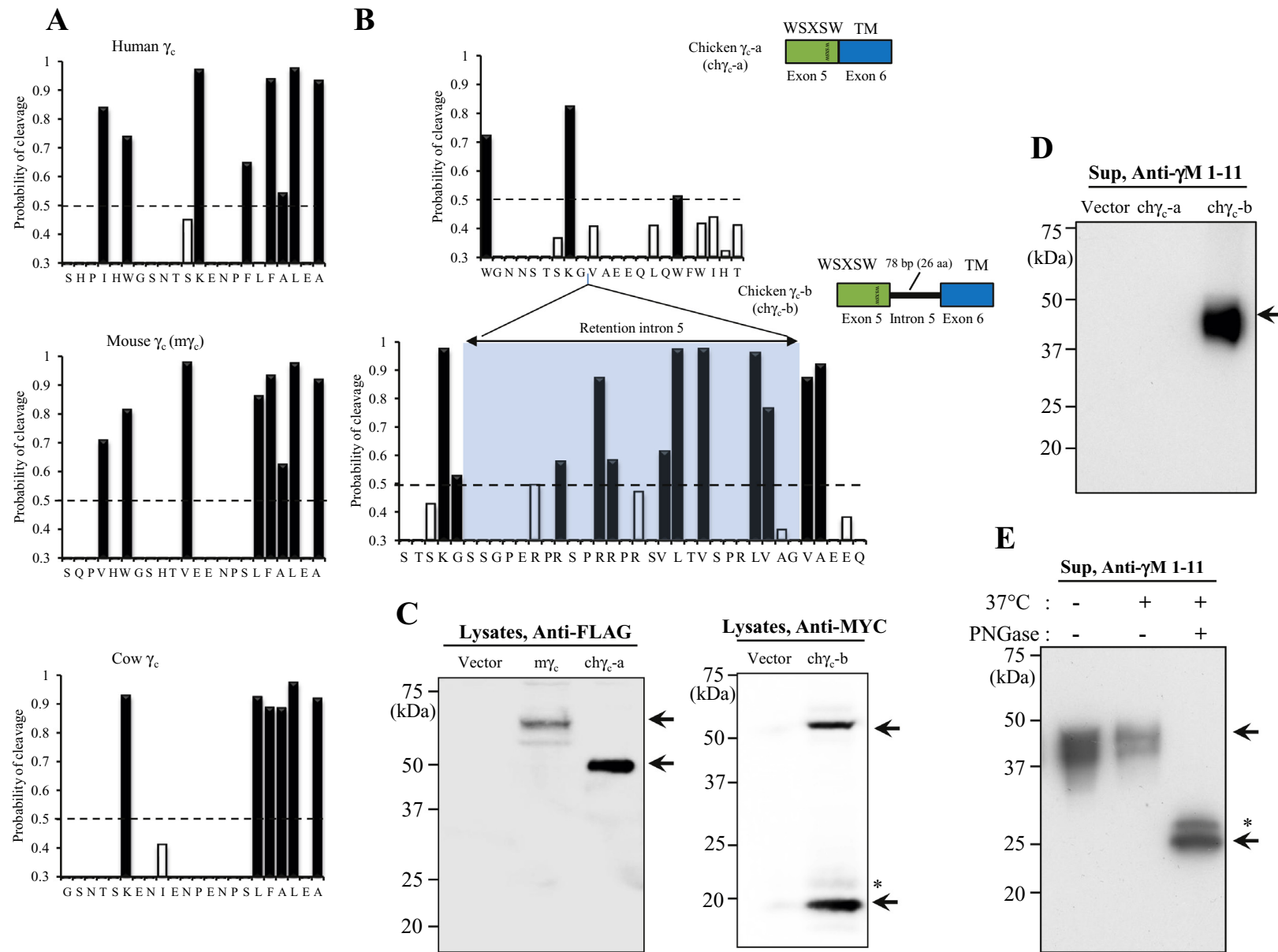
### 3.2. Detection of naturally produced $s\gamma_c$ in normal cells and cell lines

Quantitative real-time PCR (qRT-PCR) analysis was used to examine the expression of  $\gamma_c$ -a and  $\gamma_c$ -b transcripts in four chicken cell lines. The  $\gamma_c$ -a and  $\gamma_c$ -b transcripts were abundantly detected in CU91, CU205, and HD11 cells, whereas DT40 cells expressed much lower levels of  $\gamma_c$ -a and  $\gamma_c$ -b mRNA. These transcripts were not detected in COS-7 cells, which were used as a negative control (Fig. 3A). As expected, Western blotting detected specific bands corresponding to  $\gamma_c$ -a and  $\gamma_c$ -b protein in lysates and cell culture supernatants from CU91, CU205 and HD11, but not in DT40 and COS-7 (Fig. 3B and 3C). Additionally, culture supernatant from splenic mononuclear cells (SMC) of normal chickens contained these proteins. Similar to Fig. 2A, a 26 kDa protein was detected in the culture supernatants of HD11 and CU91 cells treated with PNGase-F (data not shown). These results indicate that chicken cells express naturally produced  $s\gamma_c$  forms under normal conditions.

### 3.3. Comparative analysis of $\gamma_c$ -a and $\gamma_c$ -b expression under normal, activated, and immunosuppressed conditions

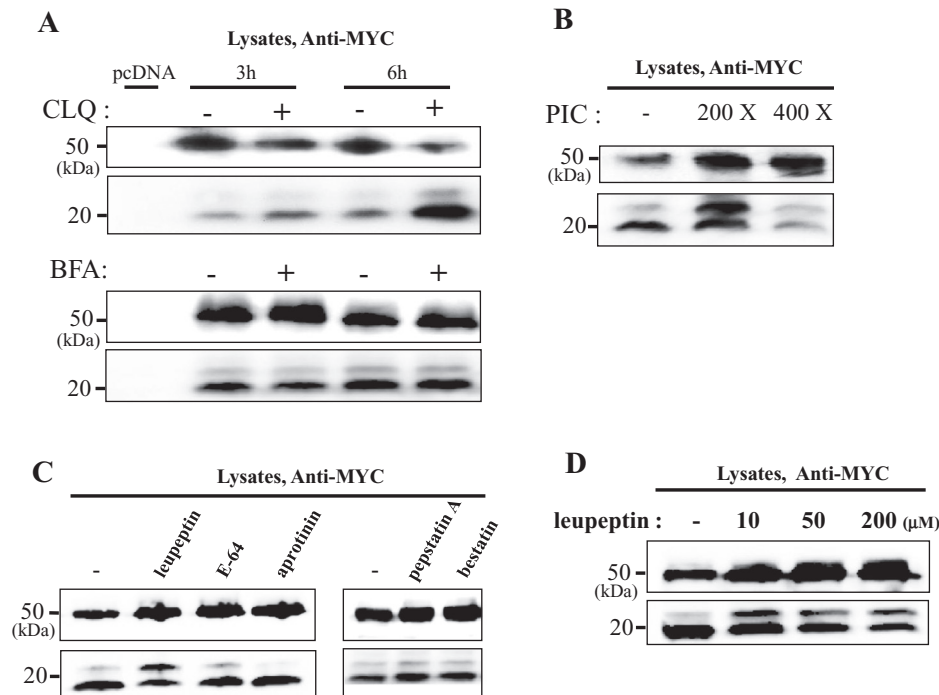
The expression level of  $\gamma_c$ -b to  $\gamma_c$ -a ( $\gamma_c$ -b/ $\gamma_c$ -a) was between 8% and 21% in normal tissues from ten-day-old chickens. The expression of  $\gamma_c$ -b was relatively high in thymus and lung, but low in heart and liver (Fig. 4A). In a day 17 embryo (E17), the level of  $\gamma_c$ -b/ $\gamma_c$ -a in thymus, bursa, and spleen was 25%, 17%, and 46%, respectively. However, dramatically reduced  $\gamma_c$ -b expression was observed in the spleen after E17 (Fig. 4B).

Next, we assessed whether mitogen treatments, parasite infection, and immunosuppressant agents affect the level of



**Fig. 1.** Cleavage predictions of  $ch\gamma_c$ -b and  $s\gamma_c$  production from  $ch\gamma_c$ -b in COS-7 cells. **A, B.** The probability of cleavage surrounding the juxtamembrane region of  $\gamma_c$  in mammals (A), as well as  $\gamma_c$ -a ( $ch\gamma_c$ -a) and  $\gamma_c$ -b ( $ch\gamma_c$ -b) in chickens (B), in the presence of intron 5 were analyzed using the NetChop 3.0 C-terminus peptide processing algorithm. The predictive program recommended a probability of cleavage above a 0.5 threshold (black bars). Low probabilities of cleavage (below 0.5) are presented in white bars. TM, transmembrane region; WSXSW, WSXSW motif. **C, D.** Lysates (C) and supernatants (D) of COS-7 cells transiently transfected with C-terminal FLAG-tagged mouse  $\gamma_c$  ( $m\gamma_c$ ) and  $ch\gamma_c$ -a, and Myc-tagged  $ch\gamma_c$ -b constructs were separated for Western blots by SDS-PAGE under reducing conditions. The specific bands were detected with the anti-tag or  $\gamma$ M1-11 antibodies.  $\gamma$ M1-11 is a monoclonal antibody directed against the extracellular domain of  $ch\gamma_c$  (Min et al., 2002). Arrows indicate specific bands representing  $m\gamma_c$  or  $ch\gamma_c$ . Asterisks indicate minor bands of  $ch\gamma_c$ -b. Data are representative of three independent experiments with similar results. **E.** The culture supernatants (50  $\mu$ l) were deglycosylated by 100 U peptide-N-glycosidase F (PNGase-F) at 37 °C for 2 h and specific bands were detected with the  $\gamma$ M1-11 monoclonal antibody. Arrows and asterisk indicate soluble  $ch\gamma_c$  and minor bands of soluble  $ch\gamma_c$ , respectively.

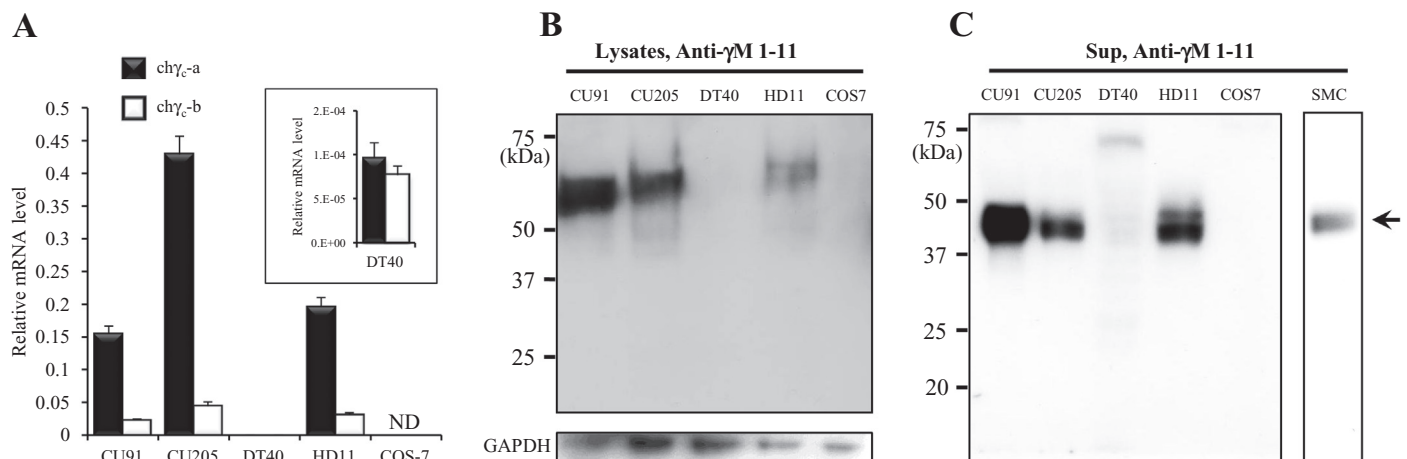




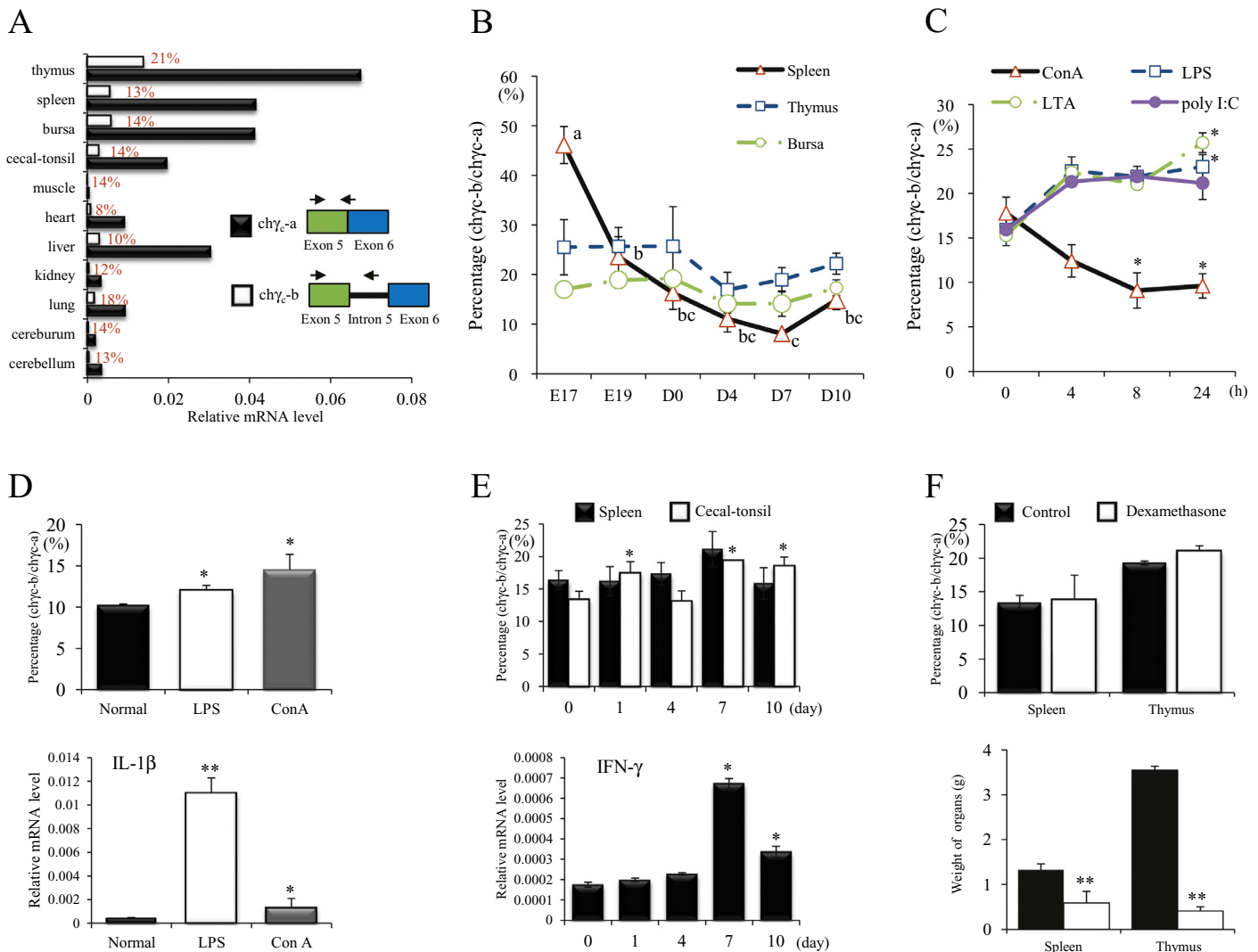
**Fig. 2.** Proteolytic ectodomain shedding of  $\text{ch}\gamma_c\text{-b}$  at the cell surface. COS-7 cells were transiently transfected with a construct expressing Myc-tagged  $\text{ch}\gamma_c\text{-b}$  for 24 h. **A.** Transfected cells were treated with 200  $\mu\text{M}$  chloroquine (CLQ) or 5  $\mu\text{g}/\text{ml}$  brefeldin A (BFA) for 3 and 6 h, followed by Western blot analysis using the anti-Myc antibody. **B.** Transfected cells were treated with the indicated concentrations of protease inhibitor cocktail (PIC) for 24 h, followed by Western blot analysis using the anti-Myc antibody. **C.** Transfected cells were treated with 50  $\mu\text{M}$  leupeptin, 5  $\mu\text{M}$  E-64, 100  $\mu\text{g}/\text{ml}$  aprotinin, 5  $\mu\text{M}$  pepstatin A or 100 nM bestatin for 24 h as indicated, followed by Western blot analysis using the anti-Myc antibody. **D.** Transfected cells were treated with the indicated dilutions of leupeptin for 24 h, followed by Western blot analysis using the anti-Myc antibody. Data are representative of two independent experiments with similar results.

$\text{ch}\gamma_c\text{-b}/\text{ch}\gamma_c\text{-a}$  *in vivo* and *in vitro* (Fig. 4C–F). Splenic lymphocytes activated with Toll-like receptor (TLR) agonists (i.e., poly I:C, LTA, and LPS) exhibited higher  $\text{ch}\gamma_c\text{-b}/\text{ch}\gamma_c\text{-a}$  levels compared to unstimulated splenic lymphocytes. Interestingly, ConA-stimulated splenic lymphocytes displayed an inverse expression pattern (Fig. 4C). However, the expression level of  $\text{ch}\gamma_c\text{-b}/\text{ch}\gamma_c\text{-a}$  *in vivo* was increased significantly in the spleen of both ConA- and LPS-inoculated groups compared to the control group (Fig. 4D). Unlike the spleen,

the cecal tonsils of *E. tenella*-infected chickens showed increased  $\text{ch}\gamma_c\text{-b}$  mRNA expression compared to normal animals (Fig. 4E). IL-1 $\beta$  and IFN- $\gamma$  expressions were examined as positive controls for ConA- and LPS stimulation, and *E. tenella* infection, respectively. Animals treated with dexamethasone, an anti-inflammatory and immunosuppressive agent, exhibited no difference in  $\text{ch}\gamma_c\text{-b}$  to  $\text{ch}\gamma_c\text{-a}$  expression in either the spleen or thymus (Fig. 4F). However, the spleen and thymus of dexamethasone-treated animals weighed less



**Fig. 3.** Detection of naturally producing  $\text{s}\gamma_c$  in cell lines and normal splenic mononuclear cells. Expression of  $\text{ch}\gamma_c\text{-a}$  and  $\text{ch}\gamma_c\text{-b}$  transcripts was analyzed in various chicken cell lines and COS-7 cells by quantitative real-time PCR. **A.** Expression levels were normalized to those of  $\beta\text{-actin}$  from the same samples. Data represent the mean plus standard error of triplicate samples. **B, C.** Expression of  $\text{ch}\gamma_c$  in whole cell lysates (**B**) and culture supernatants (**C**) from chicken lymphoid cell lines, COS-7 cells, and normal chicken splenic mononuclear cells (SMC) was assessed by Western blot using the  $\gamma\text{M}$ 1-11 monoclonal antibody. CU91 and CU205, REV-transformed lymphoblast cell lines; DT40, ALV-transformed bursal lymphoma cell line; HD11, macrophage cell line; ND, not detected. Arrows indicate soluble  $\text{ch}\gamma_c$ . Data are representative of three independent experiments with similar results.



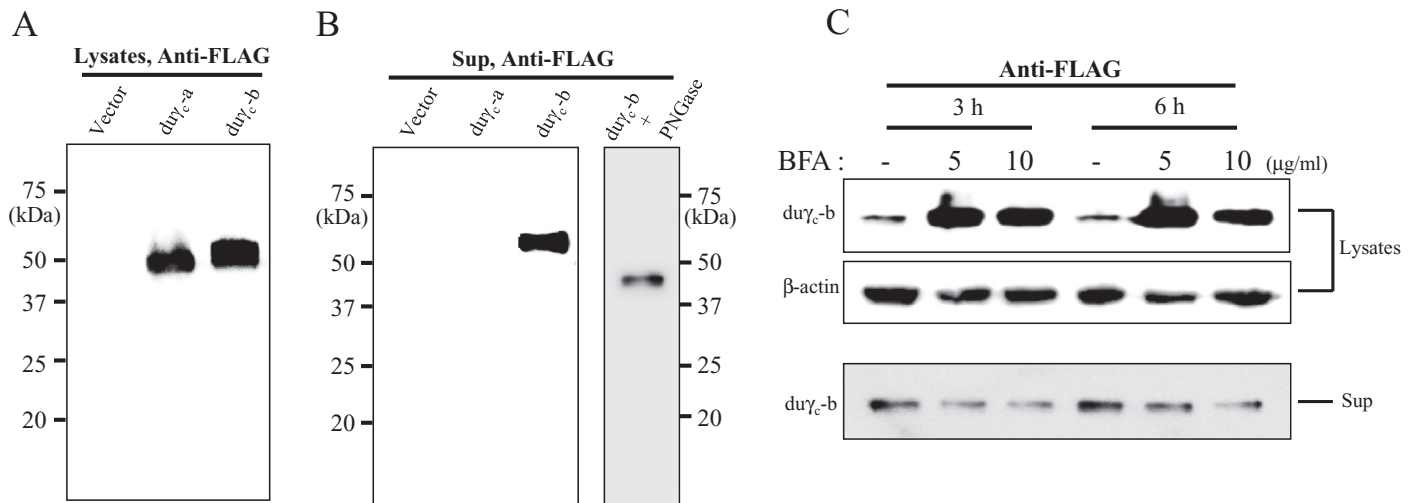
**Fig. 4.** Analysis of ch $\gamma_c$ -a and ch $\gamma_c$ -b expression under normal, activated, and immunosuppressed conditions. **A.** Expression levels of ch $\gamma_c$ -a and ch $\gamma_c$ -b transcripts in various chicken tissues as determined by quantitative real-time PCR (qRT-PCR). Tissue samples from 10-day-old chickens were pooled from five chickens. Percentage (%) indicates expression level of  $\gamma_c$ -b to  $\gamma_c$ -a. Location of the primers used is indicated by arrows. Each sample was analyzed in triplicate. Data are representative of two independent experiments with similar results. **B.** Expression levels of ch $\gamma_c$ -a and ch $\gamma_c$ -b transcripts at the indicated developmental stages. Tissue samples were collected at embryonic days 17 (E17) and 19 (E19), and at days 0 (D0), 4 (D4), 7 (D7) and 10 (D10) post-hatch. The sample was pooled from at least five eggs or chickens. Bars represent the mean  $\pm$  standard error from three independent experiments. Lowercase letters highlight statistically significant differences ( $P < 0.05$ ) according to the Dunnett multiple comparison test. **C–F.** Effect of *in vitro* and *in vivo* stimulation on ch $\gamma_c$ -a and ch $\gamma_c$ -b expression. Splenic lymphocytes (C) were isolated from 2-week-old chickens, and then activated with 10  $\mu$ g/ml ConA, 10  $\mu$ g/ml LPS, 10  $\mu$ g/ml LTA, or 25  $\mu$ g/ml Poly I:C for the indicated times. Data represent the mean  $\pm$  standard error from three independent experiments. **D.** Three-week-old chickens were injected with LPS (500  $\mu$ g/kg) or ConA (500  $\mu$ g/kg) into the wing vein. Control chickens were injected with an equal volume of PBS. After 4 h, the spleen was harvested and qRT-PCR was performed. Bars represent the mean  $\pm$  standard error from five individual chickens. **E.** Ten-day-old chickens were orally infected with  $1 \times 10^4$  sporulated *E. tenella* oocysts. Tissue samples from five chickens were collected on days 0, 1, 4, 7, and 10 post-infection and then pooled prior to performing qRT-PCR. Data represent the mean of triplicate samples, and are representative of two independent experiments with similar results. **F.** Four-week-old chickens were injected intramuscularly with dexamethasone (5 mg/kg) for 1 week and spleen and thymus were collected. Bars represent the mean  $\pm$  standard error from five individual chickens. Expression levels were normalized to those of  $\beta$ -actin from the same samples. \* $P < 0.05$  or \*\* $P < 0.01$  were considered statistically significant compared to untreated controls.

compared to normal, untreated animals. These results indicate that stimulators and pathogens, but not immunosuppressant agents, increase ch $\gamma_c$ -b to ch $\gamma_c$ -a expression. Therefore, the ratio of ch $\gamma_c$ -b to ch $\gamma_c$ -a can be differentially regulated depending on the tissue type, developmental stage, and antigen stimulation.

### 3.4. Ducks produce s $\gamma_c$ by alternative splicing

Unlike chickens, ducks most likely generate s $\gamma_c$  by alternative splicing of mRNA transcripts lacking a transmembrane region (Jeong et al., 2011). To confirm this possibility, we examined cell lysates and culture supernatants from COS-7 cells expressing

FLAG-tagged du $\gamma_c$ -a or du $\gamma_c$ -b for the presence of s $\gamma_c$  isoforms. Both isoforms were present in the cell lysate (Fig. 5A). However, FLAG-tagged du $\gamma_c$ -a, which is the duck ortholog to mammalian  $\gamma_c$ , was absent from the culture supernatant as only du $\gamma_c$ -b was detected (Fig. 5B). The du $\gamma_c$ -b isoform of approximately 56 kDa was sensitive to PNGase-F since its molecular weight was reduced to 42–44 kDa after treatment (Note the predicted size of du $\gamma_c$ -b is 41.3 kDa). Moreover, addition of brefeldin A caused a dramatic increase in du $\gamma_c$ -b expression in cell lysates, whereas s $\gamma_c$  expression was decreased in culture supernatants (Fig. 5C). These data suggest that ducks utilize a different mechanism from chickens to generate natural s $\gamma_c$  forms.



**Fig. 5.** Ducks produce  $s\gamma_c$  by alternative splicing. **A–C.** COS-7 cells transiently were transfected with a FLAG-tagged  $du\gamma_c$ -a or  $du\gamma_c$ -b construct for 24 h and then examined by Western blot. Lysates (A), culture supernatants (B), and cells (C) were treated with peptide-N-glycosidase F (PNGase-F) and brefeldin A (BFA) as indicated. The samples were separated by SDS-PAGE under reducing conditions and specific bands were detected with an anti-FLAG antibody. Data are representative of two independent experiments with similar results.

### 3.5. Mouse $\gamma_c$ and its isoforms exist mainly in cell lysates

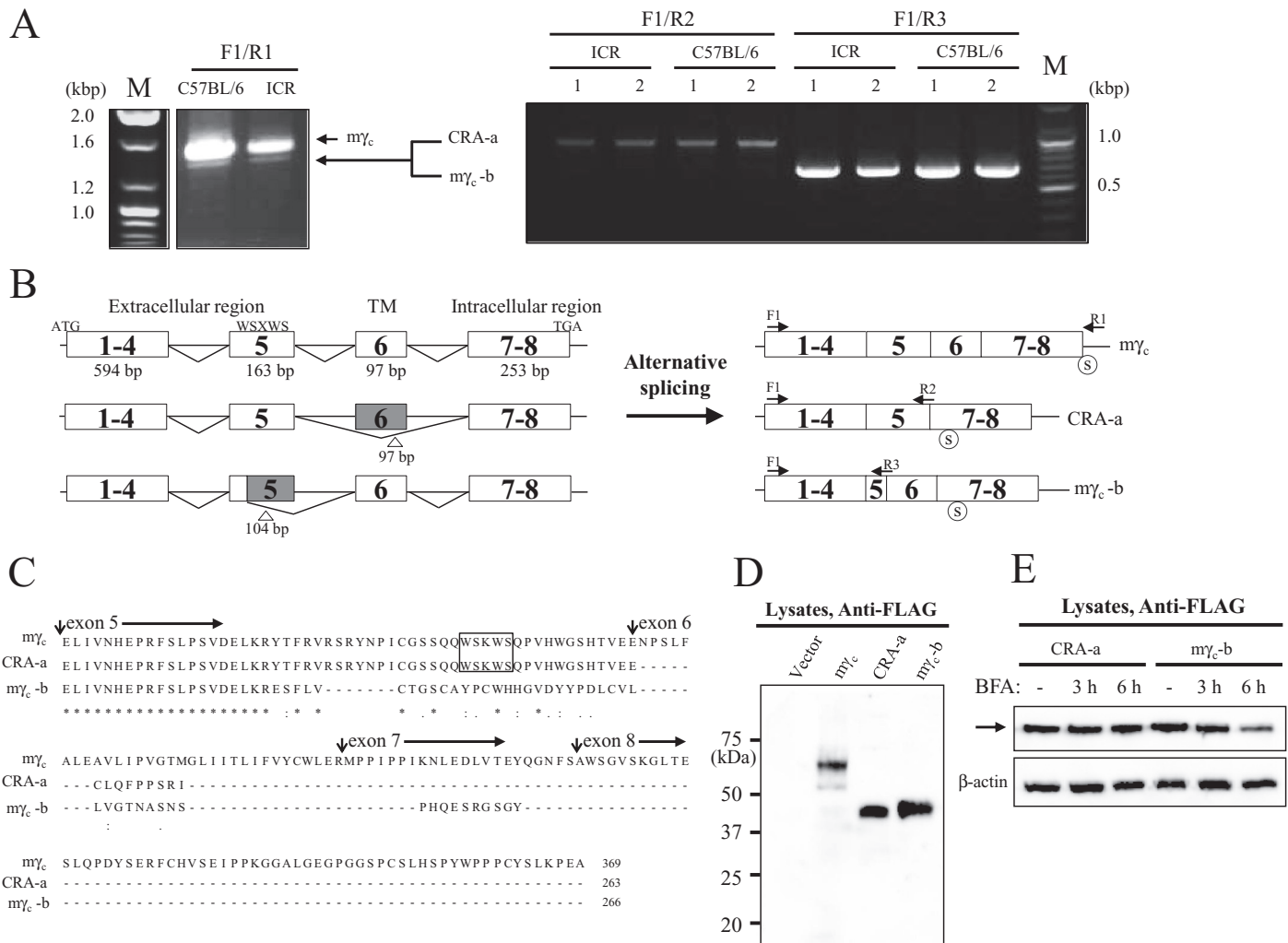
The presence of  $s\gamma_c$  was previously reported in sera from certain inbred mouse strains and stimulated immune cells. Interestingly, protease and kinase inhibitors did not suppress  $s\gamma_c$  production under these conditions (Meissner et al., 2001). A spliced IL-2R $\gamma_c$  isoform (CRA-a or  $s\gamma_c$ ) lacking exon 6 harboring a transmembrane region was detected in the mouse, rat or human (Hong et al., 2014; Olosz and Malek, 2002). However, our data show that the  $m\gamma_c$  and CRA-a isoforms predominated in the lysates, but not in culture supernatants (data not shown), of COS-7 (Fig. 6D) and HeLa cells (data not shown) transfected with FLAG-tagged  $m\gamma_c$  and CRA-a constructs. Likewise, normal COS-7 cells transfected with murine  $\gamma_c$  did not produce  $s\gamma_c$  (Meissner et al., 2001). Thus, we investigated whether additional  $\gamma_c$  isoforms exist in the mouse. Interestingly, a novel  $\gamma_c$  cDNA (hereby called  $m\gamma_c$ -b) lacking part of exon 5 and the WSXWS motif, due to alternative splicing, was detected by RT-PCR in the spleen of C57BL/6, ICR (Fig. 6A and 6B), as well as Balb/c mice (data not shown). This  $m\gamma_c$ -b gene encodes a 266 amino acid protein that lacks a transmembrane region due to a frame-shifting caused by a 104-bp deletion in exon 5 (Fig. 6B and C).  $m\gamma_c$ -b isoform was mainly detected in the lysates, but not in culture supernatants (data not shown), of COS-7 (Fig. 6D) and HeLa cells (data not shown) transfected with a FLAG-tagged  $m\gamma_c$ -b construct. In addition, brefeldin A treatment did not affect the level of CRA-a or  $m\gamma_c$ -b expression in lysates (Fig. 6E), implying that  $m\gamma_c$  and two isoforms do not produce abundantly the soluble receptors.

## 4. Discussion

Soluble cytokine receptors regulate biological events by binding and modulating the activity of target cytokines in either an antagonistic or agonistic fashion. The two major mechanisms for producing soluble receptors, alternative splicing and proteolytic cleavage, are not mutually exclusive or species-dependent (Hayashida et al., 2010; Levine, 2008). The mechanisms underlying the generation of  $s\gamma_c$  remain to be elucidated; however, several studies have investigated the production and function of  $s\gamma_c$  (Meissner et al., 2001; Nielsen et al., 1998; Nishio et al., 2001). Here, we report novel shedding mechanisms that lead to the production of  $s\gamma_c$ .

Our previous work demonstrated that avians generate the  $\gamma_c$ -b isoform harboring the fifth intron by alternative splicing (Jeong et al., 2011; Min et al., 2002). From  $\gamma_c$ -b isoforms, chickens and ducks produce  $s\gamma_c$  by proteolytic shedding and alternative splicing that results in transcripts lacking a transmembrane region, respectively. However,  $m\gamma_c$ , as well as the chicken and duck ortholog  $\gamma_c$ -a, produced little to no  $s\gamma_c$ . Given that protease and kinase inhibitors did not affect  $s\gamma_c$  generation (Meissner et al., 2001), these data suggest that normal  $\gamma_c$  do not typically give rise to  $s\gamma_c$  except in a limited number of clinical disorders (Nielsen et al., 1998; Nishio et al., 2001) and sera from certain inbred mice (Meissner et al., 2001). Previous reports suggested that the two mouse  $\gamma_c$  isoforms, CRA-a (Olosz and Malek, 2002) and  $m\gamma_c$ -b, may produce  $s\gamma_c$ ; however, our data demonstrate that they do not generate  $s\gamma_c$  in transfected COS-7 cells. Nevertheless,  $s\gamma_c$  produced from CRA-a, but not  $m\gamma_c$ -b, could be detected at very low levels with increased exposure time by Western blot (data not shown). It is noteworthy that calpains, which are calcium-dependent, non-lysosomal cysteine proteases (Saatman et al., 2010), can interact with  $\gamma_c$  to cleave intracellular PEST (proline, glutamate, serine, and threonine) motifs, suggesting that  $\gamma_c$  proteolysis by calpains could represent a regulatory mechanism for  $\gamma_c$ -dependent cytokines (Noguchi et al., 1997). Moreover,  $s\gamma_c$  was not detected in culture supernatants from normal and activated lymphocytes or in serum samples from healthy patients (Lundin et al., 2002). Taken together, these observations indicate that, unlike mice and humans, avians express abundant levels of  $s\gamma_c$  under normal conditions.

Molecules enriched from patient sera using IL-2R $\alpha$  or IL-2R $\beta$  affinity chromatography revealed the presence of proteins that bind to antibodies specific for  $\gamma_c$  (Dummer et al., 1996). Recombinant mouse  $s\gamma_c$  comprised of an extracellular WSXWS motif can inhibit cell proliferation induced by  $\gamma_c$ -dependent cytokines (Meissner et al., 2001). Thus, it can be hypothesized that chicken and duck  $s\gamma_c$  harboring an extracellular WSXWS motif possess critical biological functions. Furthermore, the cytoplasmic domain of  $\gamma_c$  contains two Src homology 2 (SH2) domains (Nelson and Willerford, 1998; Sugamura et al., 1995) that contribute to intracellular signaling by interacting with phosphotyrosine residues of various effector molecules (Malek and Castro, 2010). The intracellular region of  $ch\gamma_c$ -b contains a region with limited homology to SH2 domains (Min et al.,



**Fig. 6.** Identification of mouse  $\gamma_c$  isoforms in cell lysates. **A.** A new isoform,  $\gamma_c$ -b, was detected in different mouse species by RT-PCR. M, DNA marker. **B.** Diagram of the frame shift produced by alternative splicing that results in  $\gamma_c$ -b generation. Arrows indicate the primers used (F1, R1, R2, R3). Position of the first ATG and the stop codon (Ⓢ) are indicated. The deleted exons are indicated by gray boxes. TM; transmembrane region, WSXSW; WSXSW motif. **C.** Multiple sequence alignment of mouse  $\gamma_c$  ( $\gamma_c$ ) and differential splicing from CRA-a and  $\gamma_c$ -b. Sequences were aligned using the Clustal Omega program (<http://www.ebi.ac.uk/Tools/msa/clustalo/>). Accession numbers used in this comparison were  $\gamma_c$  (NM\_013563.3), CRA-a (EDL14151.1), and  $\gamma_c$ -b (KC815469). The WSXWS motif is boxed and exon junctions are indicated by arrows. **D.** COS-7 cells were transiently transfected with a construct expressing FLAG-tagged  $\gamma_c$ , CRA-a, or  $\gamma_c$ -b for 24 h, followed by Western blot analysis with an Anti-FLAG antibody. Cells were treated with 5  $\mu$ g/ml brefeldin A (BFA) for 3 or 6 h (E). Data are representative of three independent experiments with similar results.

2002). IL-2R $\beta$  is subject to ectodomain shedding, which generates an intracellular fragment with a role in phosphorylation, association with STAT5A, and cell proliferation (Montes de Oca et al., 2010). Considering this, we propose that an intracellular 20 kDa fragment of  $\gamma_c$ -b may be biologically functional; however, this hypothesis remains to be investigated.

Using the well-established chicken model of infection with the protozoan parasite *Eimeria* (Shirley and Lillehoj, 2012), we examined  $\gamma_c$ -b mRNA expression in the spleen and cecal tonsils of *E. tenella*-infected chickens. Cecal tonsils, but not spleen, showed upregulation of  $\gamma_c$ -b expression. It is interesting to note that *E. tenella* preferentially infects the cecum in a region-specific manner and induces mucosal immunity mediated by intestinal intraepithelial lymphocytes, resulting in protective immunity against infection (Min et al., 2004; Sharman et al., 2010; Shirley and Lillehoj, 2012).

Alternative splicing can alter the function of a gene in different tissues and developmental states by generating distinct mRNA isoforms (Hughes et al., 2012; Modrek et al., 2001). Comparative expression analysis of  $\gamma_c$ -a and  $\gamma_c$ -b mRNA revealed that  $\gamma_c$ -b expression was 21–29% higher in the spleen versus the thymus and

bursa in E17 embryos. In addition, treatment of chicken splenocytes with LPS and ConA, but not dexamethasone, led to increased  $\gamma_c$ -b mRNA expression. All TLR agonists tested upregulated  $\gamma_c$ -b mRNA in splenic lymphocytes, whereas ConA decreased expression. Considering that  $\gamma_c$  has multiple roles, including lymphocyte development, homeostasis, and cell proliferation (Alves et al., 2007; Overwijk and Schluns, 2009; Rochman et al., 2009; Vigliano et al., 2012), these observations suggest a role for  $\gamma_c$ -b in lymphocyte development and/or immune responses to environmental antigens.

Although further work is needed to clarify the physiological function of  $\gamma_c$  in regulating signaling by  $\gamma_c$ -dependent cytokines in different species, our data demonstrate that  $\gamma_c$  are naturally produced via different mechanisms, suggesting that the  $\gamma_c$  generated by proteolysis or alternative splicing could represent a different strategy by which cytokine function can be controlled.

**Conflict of interest**

The authors have no financial conflicts of interest.



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## Appendix: Supplementary data

Supplementary data associated with this article can be found, in the online version, at doi:10.1016/j.dci.2014.08.008.

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